IN THE CLAIMS

Please amend the claims as follows:

Claim 1 (Currently Amended): A method for predicting a drug transport capability of a mammalian cell, said method comprising: ~~comprising the steps of:~~

collecting a sample from a mammal,

determining a polymorphism of the nucleotide sequence of *ABCG2* gene or a polymorphism of the amino acid sequence of ABCG2 polypeptide.

Claim 2 (Original): The method of claim 1, wherein said *ABCG2* gene comprises a DNA consisting of the nucleotide sequence of SEQ ID NO:1, and said polymorphism of the nucleotide sequence is one or more of single nucleotide polymorphisms at positions selected from the group consisting of 34, 376 and 421 of SEQ ID NO:1.

Claim 3 (Original): The method of claim 2, wherein said single nucleotide polymorphism is selected from the group consisting of G34A, C376T and C421A.

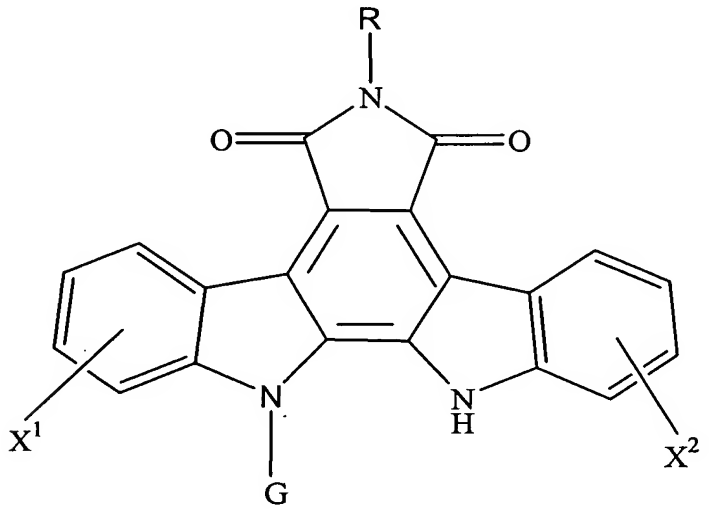
Claim 4 (Original): The method of claim 2, wherein said polymorphism of the nucleotide sequence is determined by any one of methods selected from the group consisting of a direct sequencing method, TaqMan method, invader method, mass spectrometry, RCA method and DNA chip method.

Claim 5 (Original): The method of claim 1, wherein said ABCG2 polypeptide comprises an amino acid sequence of SEQ ID NO:2, and said polymorphism of the amino acid sequence is one or more of amino acid polymorphisms at positions selected from the group consisting of 12, 126, and 141 of SEQ ID NO:2.

Claim 6 (Original): The method of claim 5, wherein said amino acid polymorphism is an amino acid substitution of Val12Met or Gln141Lys, or a deletion of the amino acid sequence downstream from the position 126 of SEQ ID NO:2.

Claim 7 (Original): The method of claim 5, wherein said polymorphism of the amino acid sequence is determined by any one of methods selected from the group consisting of mass spectrometry, two-dimensional electrophoresis method, and protein chip method.

Claim 8 (Currently Amended): The method of claim 1, ~~any one of claims 1 to 7,~~ wherein said drug is a compound represented by the ~~following general~~ formula (I):



(I)

wherein X^1 and X^2 each independently represent a hydrogen atom, halogen atom or hydroxyl group,

R represents a hydrogen atom, amino, formylamino, or lower alkylamino ~~which~~ wherein said lower alkylamino may be substituted with any one selected from the group consisting of one to three hydroxyl ~~group(s)~~, a pyridyl ~~group~~ optionally having substituent(s), and a thienyl ~~group~~ optionally having substituent(s), and

G represents a pentose group or hexose group or derivative thereof which may be substituted with an amino group.

Claim 9 (Original): A polynucleotide having a single nucleotide polymorphism(s) at one or more position(s) selected from the group consisting of 34, 376 and 421 of SEQ ID NO:1, said polynucleotide comprising any one of the positions of said single nucleotide polymorphisms and consisting of at least 10 contiguous nucleotides of SEQ ID NO:1, or a complementary polynucleotide thereto.

Claim 10 (Original): The polynucleotide of claim 9, wherein said single nucleotide polymorphism is selected from the group consisting of G34A, C376T, C421A and single nucleotide polymorphisms complementary thereto.

Claim 11 (Original): A polynucleotide having one or more of the nucleotide polymorphisms in the polynucleotide sequence of SEQ ID NO:1, said polymorphism selected from the group consisting of nucleotide polymorphisms by which the translated amino acid at position 12 is methionine, one at position 126 is stop codon, and one at position 141 is lysine, and consisting of at least 10 contiguous nucleotides including one or more of nucleotides located at the site of said nucleotide polymorphisms, or a complementary polynucleotide thereto.

Claim 12 (Original): A pair of PCR primers which specifically hybridize to *ABCG2* gene, and amplify a DNA fragment of a portion of said gene, wherein the amplified DNA fragment comprises a nucleotide(s) at position 34, 376 or 421 of SEQ ID NO:1

Claim 13 (Original): The pair of PCR primers of claim 12, said pair of PCR primers selected from the group of:

SEQ ID NO:5 and SEQ ID NO:6; SEQ ID NO:9 and SEQ ID NO:10; and SEQ ID NO:11 and SEQ ID NO:12.

Claim 14 (Original): A polynucleotide which specifically hybridizes to *ABCG2* gene, and which is capable of detecting a polymorphism(s) of *ABCG2* gene at position 34, 376 or 421 of SEQ ID NO:1.

Claim 15 (Original): The polynucleotide of claim 14, which is capable of using in any one of methods selected from the group consisting of a direct sequencing method, TaqMan method, invader method, mass spectrometry, RCA method and DNA chip method.

Claim 16 (Original): A polypeptide having polymorphic mutation(s) to ABCG2 protein defined in the following (a) or (b), said polypeptide is a polymorphic mutant wherein one or both of amino acids at positions 12 and 141 of SEQ ID NO:2 are substituted with other amino acid(s), a polypeptide fragment comprising said substituted amino acid and at least 10 contiguous amino acid residues of said polymorphic mutant, or a polypeptide wherein the amino acid sequence downstream from the position 126 of SEQ ID NO:2 is deleted:

(a) a human ABCG2 polypeptide consisting of an amino acid sequence of SEQ ID No: 2,

(b) an isopolypeptide of (a) consisting of an amino acid sequence of SEQ ID NO:2, wherein one or several amino acids except for the amino acids at positions 12, 126 and 141, are deleted, substituted or added, and having a drug transport capability.

Claim 17 (Original): An antibody which specifically binds to the mutant ABCG2 polypeptide of claim 16.

Claim 18 (Original): A transformed cell which expresses an polypeptide having polymorphic mutation(s) to ABCG2 protein defined in the following (a) or (b), said polymorphic mutation(s) being one or both of amino acid substitutions Val12Met and Gln141Lys of the amino acid sequence of SEQ ID NO:2:

(a) a human ABCG2 polypeptide consisting of an amino acid sequence of SEQ ID NO:2,

(b) an isopolypeptide of (a) consisting of an amino acid sequence of SEQ ID NO:2, wherein one or several amino acids except for the amino acids at positions 12, 126 and 141, are deleted, substituted or added, and having a drug transport capability.

Claim 19 (Original): A method for measuring a drug transport capability using the transformed cell of claim 18.

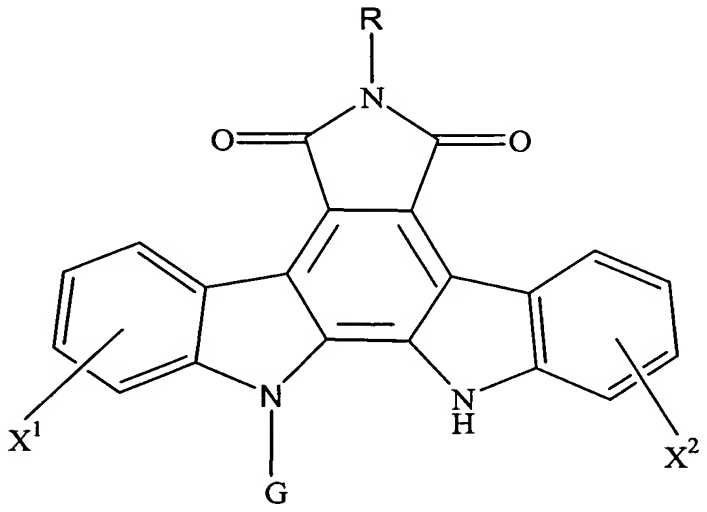
Claim 20 (Currently Amended): A method for diagnosing a drug sensitivity, said method comprising ~~the steps of~~:

analyzing a biological sample from a subject, and determining the presence or absence of a polynucleotide ~~of any one of claims 9 to 11,~~ having a single nucleotide polymorphism(s) at one or more position(s) selected from the group consisting of 34, 376 and 421 of SEQ ID NO:1, said polynucleotide comprising any one of the positions of said single nucleotide polymorphisms and consisting of at least 10 contiguous nucleotides of SEQ ID NO:1, or a complementary polynucleotide thereto; or

a polynucleotide having one or more of the nucleotide polymorphisms in the polynucleotide sequence of SEQ ID NO:1, said polymorphism selected from the group consisting of nucleotide polymorphisms by which the translated amino acid at position 12 is methionine, one at position 126 is stop codon, and one at position 141 is lysine, and consisting of at least 10 contiguous nucleotides including one or more of nucleotides located at the site of said nucleotide polymorphisms, or a complementary polynucleotide thereto; or

a polypeptide of claim 16.

Claim 21 (Currently Amended): The method of claim 20, wherein the subject having said polynucleotide and/or said polypeptide is suggested to be sensitive to the compound represented by the ~~following general~~ formula (I):



(I)

wherein X^1 and X^2 each independently represent a hydrogen atom, halogen atom or hydroxyl group,

R represents a hydrogen atom, amino, formylamino, or lower alkylamino ~~which~~ wherein said lower alkylamino may be substituted with any one selected from the group consisting of one to three hydroxyl ~~group(s)~~, a pyridyl ~~group~~ optionally having substituent(s), and a thienyl ~~group~~ optionally having substituent(s), and

G represents a pentose group or hexose group or derivative thereof which may be substituted with an amino group.

Claim 22 (Currently Amended): A kit for diagnosing a drug sensitivity comprising one or more of the following (a) to (f):

(a) a polynucleotide having a single nucleotide polymorphism(s) at one or more position(s) selected from the group consisting of 34, 376 and 421 of SEQ ID NO:1, said polynucleotide comprising any one of the positions of said single nucleotide polymorphisms and consisting of at least 10 contiguous nucleotides of SEQ ID NO:1, or a complementary polynucleotide thereto; or

a polynucleotide having one or more of the nucleotide polymorphisms in the polynucleotide sequence of SEQ ID NO:1, said polymorphism selected from the group consisting of nucleotide polymorphisms by which the translated amino acid at position 12 is methionine, one at position 126 is stop codon, and one at position 141 is lysine, and consisting of at least 10 contiguous nucleotides including one or more of nucleotides located at the site of said nucleotide polymorphisms, or a complementary polynucleotide thereto; ~~the polynucleotide of any one of claims 9 to 11,~~

(b) a pair of PCR primers which specifically hybridize to *ABCG2* gene, and amplify a DNA fragment of a portion of said gene, wherein the amplified DNA fragment comprises a nucleotide(s) at position 34, 376 or 421 of SEQ ID NO:1; ~~the pair of primers of claim 12 or 13,~~

(c) a polynucleotide which specifically hybridizes to *ABCG2* gene, and which is capable of detecting a polymorphism(s) of *ABCG2* gene at position 34, 376 or 421 of SEQ ID NO:1; ~~the polynucleotide of claim 14 or 15,~~

(d) a polypeptide having polymorphic mutation(s) to ABCG2 protein defined in the following (i) or (ii), said polypeptide is a polymorphic mutant wherein one or both of amino acids at positions 12 and 141 of SEQ ID NO:2 are substituted with other amino acid(s), a polypeptide fragment comprising said substituted amino acid and at least 10 contiguous amino acid residues of said polymorphic mutant, or a polypeptide wherein the amino acid sequence downstream from the position 126 of SEQ ID NO:2 is deleted:

(i) a human ABCG2 polypeptide consisting of an amino acid sequence of SEQ ID No: 2,

(ii) an isopolypeptide of (i) consisting of an amino acid sequence of SEQ ID NO:2, wherein one or several amino acids except for the amino acids at positions 12, 126 and 141, are deleted, substituted or added, and having a drug transport capability; ~~the polypeptide of claim 16,~~

(e) ~~the~~ said antibody of claim 17, and

(f) a transformed cell which expresses an polypeptide having polymorphic mutation(s) to ABCG2 protein defined in the following (i) or (ii), said polymorphic mutation(s) being one or both of amino acid substitutions Val12Met and Gln141Lys of the amino acid sequence of SEQ ID NO:2:

(i) a human ABCG2 polypeptide consisting of an amino acid sequence of SEQ ID NO:2,

(ii) an isopolypeptide of (i) consisting of an amino acid sequence of SEQ ID NO:2, wherein one or several amino acids except for the amino acids at positions 12, 126 and 141, are deleted, substituted or added, and having a drug transport capability. ~~the transformed cell of claim 18.~~

Claim 23 (Currently Amended): A computer system for analyzing data of ABCG2 polymorphism, comprising:

(a) an input/output device,

(b) a memory ~~containing~~ comprising the polymorphism data, and

(c) a central processing unit.